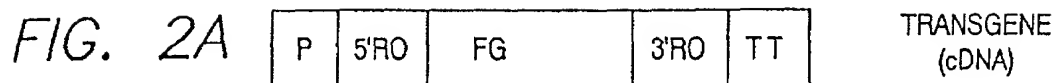


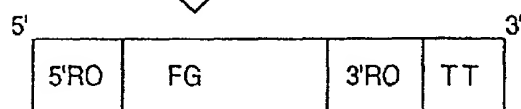
- GENOMIC RNA
- ◆ AMBER STOP CODON (READTHROUGH SITE)
- SUBGENOMIC PROMOTER
- SUBGENOMIC mRNA
- ↑↓ TRANSLATION
- ▣ VIRAL PROTEIN
- REPLICATION ORIGINS
- R REPLICASE PROTEINS
- M MOVEMENT PROTEIN
- C CAPSID PROTEIN
- 1 cm ~ 0.6 kb

FIG. 1

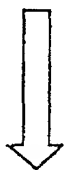


TRANSCRIPTION

FIG. 2B

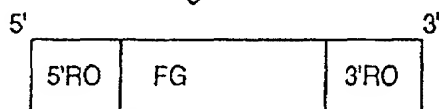


TRANSCRIPT (RNA)



RNA PROCESSING
AND
RNA REPLICATION

FIG. 2C



REPLICON (RNA)

P = PROMOTER

5'RO = 5' REPLICATION ORIGIN

FG = SEQUENCE CODING FOR FOREIGN GENE AS WELL AS OTHER SEQUENCES.
DOES NOT CODE FOR COMPLETE SET OF VIRAL REPLICATION PROTEINS
REQUIRED FOR REPLICATION.

3' RO = 3' REPLICATION ORIGIN

TT = TRANSCRIPTION TERMINATION SEQUENCE

FIG. 2

FIG. 2A

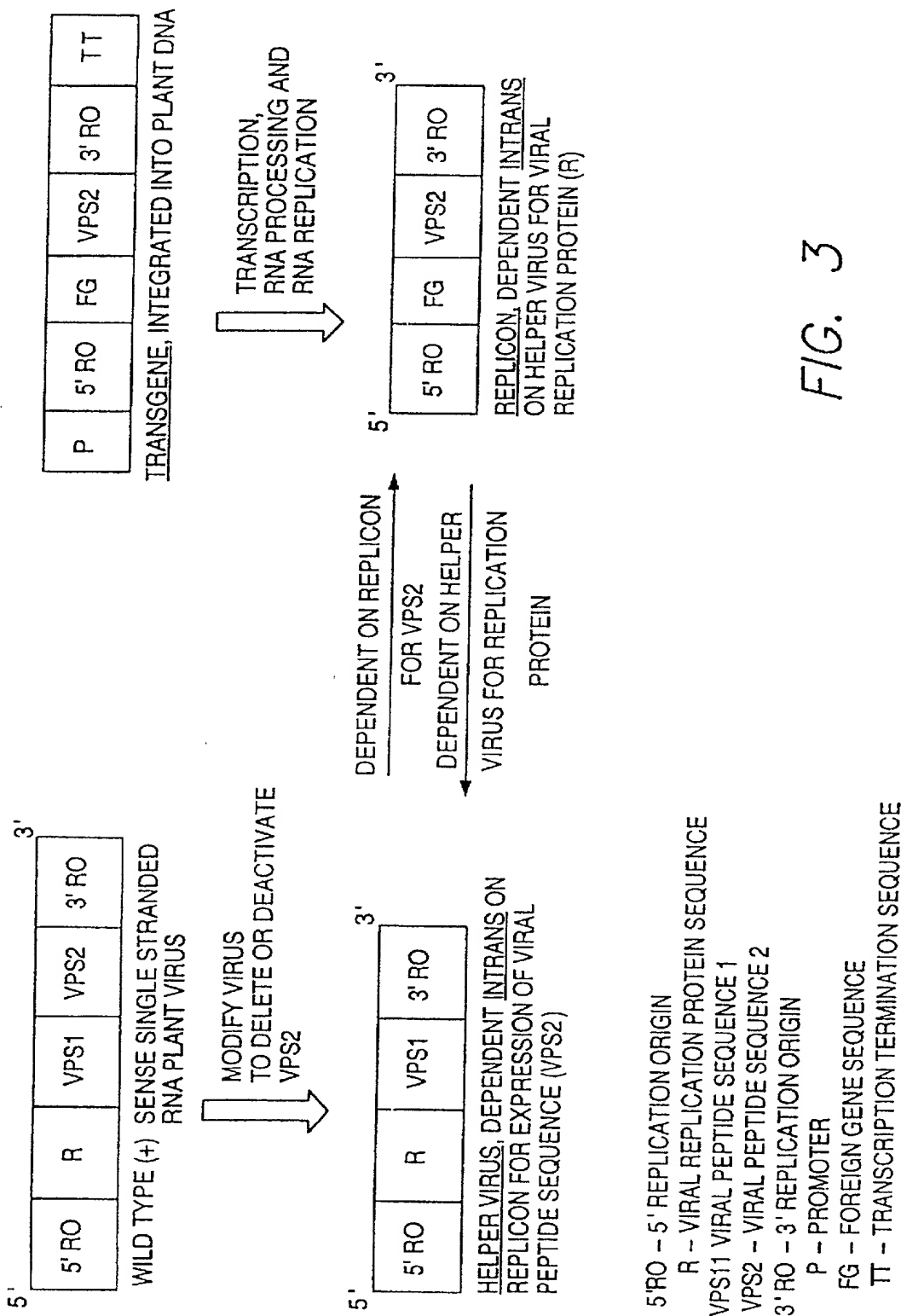


FIG. 3

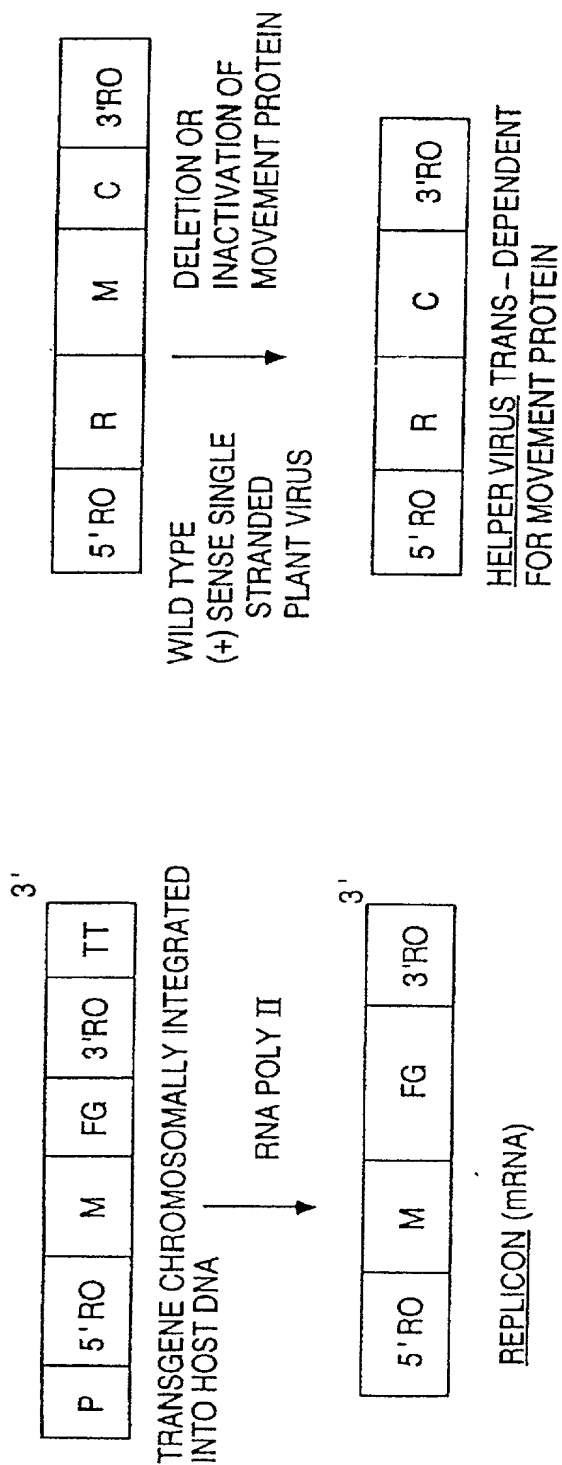
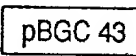
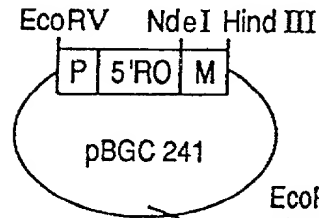
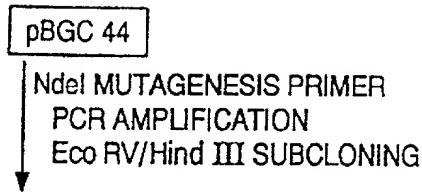


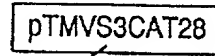
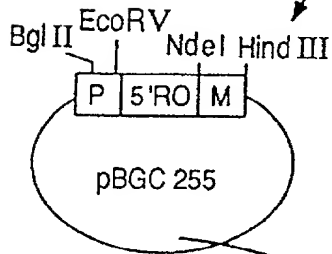
FIG. 4

R: REPLICATION PROTEINS GENES
M: MOVEMENT PROTEIN GENE
RO: REPLICATION ORIGIN
RT: RIBOZYME TERMINATION REGION
CAT: CHLORAMPHENICOL ACETYL TRANSFERASE
P: 35S PROMOTER

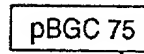


EcoRV
Hind III
(Fragment)

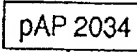
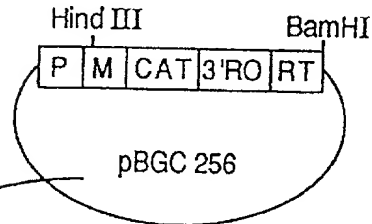
EcoRV/Hind III



Hind III / Nsi I
(Fragment)



Hind III/
Nsi I



Bam HI

Bgl II/
Hind III
(Fragment)

Hind III/Bam HI
(Fragment)

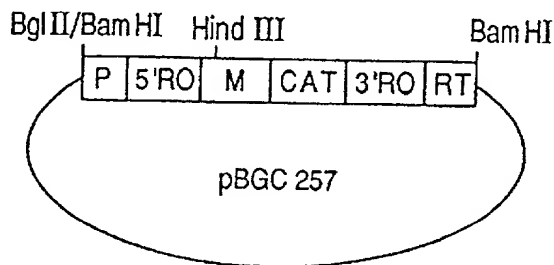


FIG. 5

FIG. 6-2

	736	GGG	AAA	AAU	AGU	AGU	AAU	GAU	CGG	UCA	GUG	CCG	AAC	AAG	AAC	UAU	780
	233	G	K	N	S	S	N	D	R	S	V	P	N	K	N	Y	237
50																	
	781	AGA	AAU	GUU	AAG	GAU	UUU	GGA	GGA	AUG	AGU	UUU	AAA	AAG	AAU	AAU	825
	238	R	N	V	K	D	F	G	G	M	S	F	K	K	N	N	252
	826	UUA	AUC	GAU	GAU	GAU	UCG	GAG	GCU	ACU	GUC	GCC	GAA	UCG	GAU	UCG	870
	253	L	I	D	D	D	S	E	A	T	V	A	E	S	D	S	267
5	871	UUU	UAA	auacgcucgacgagauuuucaggagcuaaggaagcuaaa										AUG	GAG	AAA	924
	263	F	*											M	E	K	3
	925	AAA	AUC	ACU	GGA	UAU	ACC	ACC	GUU	GAU	AUA	UCC	CAA	UCG	CAU	CGU	969
	4	K	I	T	G	Y	T	T	V	D	I	S	Q	S	H	R	18
10																	
	970	AAA	GAA	CAU	UUU	GAG	GCA	UUU	CAG	UCA	GUU	GCU	CAA	UGU	ACC	UAU	1014
	19	K	E	H	F	E	A	F	Q	S	V	A	Q	C	T	Y	33
																	T
	1015	AAC	CAG	ACC	GUU	CAG	CUG	GAU	AUU	ACG	GCC	UUU	UUA	AAG	ACC	GUA	1059
15	34	N	Q	T	V	Q	L	D	I	T	A	F	L	K	T	V	48
																	P
	1060	AAG	AAA	AAU	AAG	CAC	AAG	UUU	UAU	CCG	GCC	UUU	AUU	CAC	AUU	CUU	1104
	49	K	K	N	K	H	K	F	Y	P	A	F	I	H	I	L	63
																	E
20	1105	GCC	CGC	CUG	AUG	AAU	GCU	CAU	CCG	GAA	UUC	CGU	AUG	GCA	AUG	AAA	1149
	64	A	R	L	M	N	A	H	P	E	F	R	M	A	M	K	78
																	N
	1195	GUU	UUC	CAU	GAG	CAA	ACU	GAA	ACG	UUU	UCA	UCG	CUC	UGG	AGU	GAA	1239
	94	V	F	H	E	Q	T	E	T	F	S	S	L	W	S	E	108
25																	
	1240	UAC	CAC	GAC	GAU	UUC	CGG	CAG	UUU	CUA	CAC	AUA	UAU	UCG	CAA	GAU	1284
	109	Y	H	D	D	F	R	Q	F	L	H	I	Y	S	Q	D	123
	1285	GUG	GCG	UGU	UAC	GGU	GAA	AAC	CUG	GCC	UAU	UUC	CCU	AAA	GGG	UUU	1329
30	124	V	A	C	Y	G	E	N	L	A	Y	F	P	K	G	F	138
	1330	AUU	GAG	AAU	AUG	UUU	UUC	GUC	UCA	GCC	AAU	CCC	UGG	GUG	AGU	UUC	1374
	139	I	E	N	M	F	F	V	S	A	N	P	W	V	S	F	153
35	1375	ACC	AGU	UUU	GAU	UUA	AAC	GUG	GCC	AAU	AUG	GAC	AAC	UUC	UUC	GCC	1419
	154	T	S	F	D	L	N	V	A	N	M	D	N	F	F	A	168
	1420	CCC	GUU	UUC	ACC	AUG	GGC	AAA	UAU	UAU	ACG	CAA	GGC	GAC	AAG	GUG	1464
	169	P	V	F	T	M	G	K	Y	Y	T	Q	G	D	K	V	183
40																	

0990339 004401
 "T4TBD" 63206660

FIG. 6-3

	1465	CUG	AUG	CCG	CUG	GCG	AUU	CAG	GUU	CAU	CAU	GCC	GUC	UGU	GAU	GGC	1509	
	184	L	M	P	L	A	I	Q	V	H	H	A	V	C	D	G	198	
	1510	UUC	CAU	GUC	GGC	AGA	AUG	CUU	AAU	GAA	UUA	CAA	CAG	UAC	UGC	GAU	1554	
45	199	F	H	V	G	R	M	L	N	E	L	Q	Q	Y	C	D	213	
	1555	GAG	UGG	CAG	GGC	GGG	GCG	UAA	uuuuuuu	aaggc	aguuau	uggug	cccuua	aac			1607	
	214	E	W	Q	G	G	A	*									220	↓
	1608	gccuggug	cuacg	ccuga	auaag	ugaua	auaag	cggau	gaau	ggcaga	aaau	cgucg	agg				1667	
50	1668	guaguca	aagau	gcaua	auaaaa	aacgga	uugug	uccgua	aucaca	caggug	cgua	cga					1727	
	1728	aacgcau	agugu	uuuu	ccucca	cuuaaa	ucgaag	ggugug	ucuugg	aucgcg	cgguc						1787	
	1788	aaangua	uauggu	cauau	acaucc	gcaggc	acgua	auaa	agcgag	gggu	ucgaa	uccc					1847	
	1848	ccguu	accccc	gguag	gggcc	cca											1870	

FIG. 6-3